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TABLE 1

M PPKTPRKTAATAAAAAEPPAPPPEEDPE	(34)
QDSGPEDLPLVRLEFEETEEDFTALCQKLKIPDHVRERA	(74)
WLTWEKVSSVDGVLGGYIQKKKELWGICIFIAAVDLDEM	(114)
FTFTTELQKNIEISVHKFFNLLKEIDTSTKVDNAMSRLKK	(154)
YDVLFALFSKLERTCELIYLTPSSSISTEINSALVLKV	(194)
WITFLLAKGEVLQMEDDLVISFQLNLCVLDYFIKLSPPML	(234)
LKEPYKTAVIPINGSRTPRGQMRSARIAKQLENDTRII	(274)
EVLCKEHECNIDEVKNVYFKNFIPFMNSLGLVTSNGLPEV	(314)
ENLSKRYEEIYLKNKDLDARLFLDHDKTLQTDIDSFETQ	(354)
RTPRKSNLDEEVNVIPHTPVRTVMNTIQQLMMILNSASD	(394)
QPSENLISYFNCTVNPKESILKRVKDIFYIFKEKFAKAV	(434)
GQGCVEIGSQRYKLGVRLYYRVMESMLKSEEERLSIQNFS	(474)
KLLNDNIFHMSLLACALEVVMATYSRSTSQNLDGTDLSF	(514)
PWILNVNLKAFDFYKVIIESFIKAEGNLTREMIKHLERCE	(554)
HRIMESLAWLSDSPLFDLIKQSKDREGPTDHLESACPLNL	(594)
PLQNNHTAADMYLSPVRSPKKKGSTRVNSTANAETQATS	(634)
AFQTQKPLKSTSLSLFYKKVYRLAYRLNLTLCERLLSEHP	(674)
ELEHIIWTLFQHTLQNEYELMRDRHLDQIMMCSMYGICKV	(714)
KNIDLKFKIIVTAYKDLPHAVQETFKRVLIKEEYDSIIV	(754)
FYNSVFMQRLKTNILQYASTRPTLSPIPHIPRSPYKFPS	(794)
SPLRIPGGNIYIISPLKSPYKISEGLPTPTKMTPRSRILVS	(834)
IGESFGTSEKFQKINQMVCNSDRVLRSAEGSNPPKPLKK	(874)
LRFDIEGSDEADGSKHLPGESKFQQKLAEMTSTRTRMVKQ	(914)
KMNDMSMTSNKEEK	(928)

single-letter abbreviations for the amino acid residues are:
 A, Ala; C, Cys; D, Asp; E, Gly; F, Phe; G, Gly; H, His;
 I, Ile; K, Lys; L, Leu; M, Met; N, Asn; P, Pro; Q, Gln;
 R, Arg; S, Ser; T, Thr; V, Val; W, Trp; and Y, Tyr.--

Please replace paragraph [153] beginning at page 27, line 15, with the following:

[153] --The amino acid sequence (Table 1; SEQ ID NO:2) is written in the abbreviation code recognized in the art. Single-letter abbreviations for the amino acid residues are: A = Alanine, C = Cysteine, D = Aspartic acid, E = Glutamic Acid, F = Phenylalanine, G = Glycine, H = Histidine, I = Isoleucine, K = Lysine, L = Leucine, M = Methionine, N =

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Asparagine, P = Proline, Q = Glutanine, R = Arginine, S = Serine, T = Threonine, V = Valine, W = Tryptophane and Y = Tyrosine.--

Please replace paragraph [225] beginning at page 27, line 15, with the following:

[225] --Pending U.S. patent application Serial No. 108,748 discloses and claims the RB gene and its clone. The RB gene and its clone had the nucleotide and amino acid sequences sequence depicted in Table 4 Table 2 (SEQ ID NOS:1 and 2).

TABLE 4

TTCCGGTTTT TCTCAGGGGA CGTTGAAATT ATTTTGTAA CGGGAGTCGG GAGAGGACGG	60
GGCGTCCCC GCGTGCAGCGC GCGTCGTCCT CCCCGCGCT CCTCCACAGC TCGCTGGCTC	120
CCGCCGCGGA AAGGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC	171
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala	
1 5 10	
ACC GCC GCC GCT GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC	219
Thr Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro	
15 20 25	
CCT CCT GAG GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT	267
Pro Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro	
30 35 40	
CTC GTC AGG CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA	315
Leu Val Arg Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala	
45 50 55	
TTA TGT CAG AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG	363
Leu Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp	
60 65 70 75	
TTA ACT TGG GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT	411
Leu Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr	
80 85 90	
ATT CAA AAG AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA	459
Ile Gln Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala	
95 100 105	
GTT GAC CTA GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC	507
Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn	
110 115 120	

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ATA GAA ATC AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp	555
125 130 135	
ACC AGT ACC AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr	603
140 145 150 155	
GAT GTA TTG TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu	651
160 165 170	
ATA TAT TTG ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT Ile Tyr Leu Thr Gln Pro Ser Ser Ile Ser Thr Glu Ile Asn Ser	699
175 180 185	
GCA TTG GTG CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly	747
190 195 200	
GAA GTA TTA CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG Glu Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met	795
205 210 215	
CTA TGT GTC CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC Leu Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu	843
220 225 230 235	
AAA GAA CCA TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA Lys Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg	891
240 245 250	
ACA CCC AGG CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu	939
255 260 265	
GAA AAT GAT ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys	987
270 275 280	
AAT ATA GAT GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe	1035
285 290 295	
ATG AAT TCT CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu	1083
300 305 310 315	
AAT CTT TCT AAA CGA TAC GAA ATT TAT CTT AAA AAT AAA GAT CTA Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu	1131
320 325 330	

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GAT GCA AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT	1179
Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser	
335	340
	345
ATA GAC AGT TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT	1227
Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp	
350	355
	360
GAA GAG GTG AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG	1275
Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met	
365	370
	375
AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA	1323
Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln	
380	385
	390
	395
CCT TCA GAA AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA	1371
Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro	
400	405
	410
AAA GAA AGT ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA	1419
Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys	
415	420
	425
GAG AAA TTT GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA	1467
Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser	
430	435
	440
CAG CGA TAC AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC	1515
Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser	
445	450
	455
ATG CTT AAA TCA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA	1563
Met Leu Lys Ser Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys	
460	465
	470
	475
CTT CTG AAT GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT	1611
Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu	
480	485
	490
GAG GTT GTA ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT	1659
Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp	
495	500
	505
TCT GGA ACA GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA	1707
Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu	
510	515
	520
AAA GCC TTT GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA	1755
Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu	
525	530
	535

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GGC AAC TTG ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT	1803
Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His	
540 545 550 555	
CGA ATC ATG GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT	1851
Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp	
560 565 570	
CTT ATT AAA CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA	1899
Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu	
575 580 585	
TCT GCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA	1947
Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala	
590 595 600	
GAT ATG TAT CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT	1995
Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr	
605 610 615	
ACG CGT GTA AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC	2043
Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala	
620 625 630 635	
TTC CAG ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT	2091
Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr	
640 645 650	
AAA AAA GTG TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA	2139
Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu	
655 660 665	
CGC CTT CTG TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT	2187
Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu	
670 675 680	
TTC CAG CAC ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT	2235
Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His	
685 690 695	
TTG GAC CAA ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG	2283
Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys	
700 705 710 715	
AAT ATA GAC CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT	2331
Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu	
720 725 730	
CCT CAT GCT GTT CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG	2379
Pro His Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu	
735 740 745	
GAG TAT GAT TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA	2427

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Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg			
750	755	760	
CTG AAA ACA AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG		2475	
Leu Lys Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu			
765	770	775	
TCA CCA ATA CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA		2523	
Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser			
780	785	790	795
CCC TTA CGG ATT CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT		2571	
Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser			
800	805	810	
CCA TAT AAA ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA		2619	
Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro			
815	820	825	
AGA TCA AGA ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG		2667	
Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu			
830	835	840	
AAG TTC CAG AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC		2715	
Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu			
845	850	855	
AAA AGA AGT GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA		2763	
Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu			
860	865	870	875
CGC TTT GAT ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC		2811	
Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu			
880	885	890	
CCA GGA GAG TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT		2859	
Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr			
895	900	905	
CGA ACA CGA ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA		2907	
Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser			
910	915	920	
AAC AAG GAA GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT		2962	
Asn Lys Glu Glu Lys			
925			
GGATTCATTG TCTCTCACAG ATGTGACTGT AT		2994	

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TABLE 4

TTCCGGTTTT	TCTCAGGGGA	CGTTGAAATT	ATTTTCTAA	CGGGACTCGG	GACAGGACGG	60											
GGCGTCCCCC	CCCTGGGGCC	CGCTCGTCCT	CCCCGGGCGT	CCTCCACAGC	TCGCTGGCTC	120											
CCCCCCCCGA	AACGGGTC	ATC	CCC	CCC	AAA	ACC	CCC	CGA	AAA	ACG	CCC	CCC	171				
		Met	Pro	Pro	Lys	Thr	Pro	Arg	Lys	Thr	Ala	Ala					
		1				5				10							
ACC	CCC	CCC	CCT	CCC	CCC	GCG	CAA	CCC	CCC	GCA	CCC	CCC	CCC	219			
Thr	Ala	Ala	Ala	Ala	Ala	Glu	Pro	Pro	Pro	Ala	Pro	Pro	Pro				
		15				20				25							
CCT	CCC	TAC	GAG	GAC	CCA	GAG	CAG	GAC	AGC	CCC	CCC	GAG	GAC	CTG	267		
Pro	Pro	Glu	Glu	Asp	Pro	Glu	Gln	Asp	Ser	Gly	Pro	Glu	Asp	Leu	Pro		
		30				35				40							
CTC	GTC	AGG	CTT	GAG	TTT	GAA	CAA	ACA	CAA	GAA	CCT	CAT	TTT	ACT	GCA	315	
Leu	Val	Arg	Leu	Glu	Phe	Glu	Glu	Thr	Glu	Glu	Pro	Asp	Phe	Thr	Ala		
		45				50				55							
TTA	TCT	CAG	AAA	TTA	AAG	ATA	CCA	CAT	CAT	CTC	AGA	GAC	AGA	GCT	TGG	363	
Leu	Cys	Gln	Lys	Leu	Lys	Ile	Pro	Asp	His	Val	Arg	Glu	Arg	Ala	Trp		
		60				65				70				75			
TTA	ACT	TGG	GAC	AAA	CTT	TCA	TCT	CTG	GAT	GGG	GTA	TTG	GGG	CGT	TAT	411	
Leu	Thr	Trp	Glu	Lys	Val	Ser	Ser	Val	Asp	Gly	Val	Leu	Gly	Gly	Tyr		
		80				85				90							
ATT	CAA	AAG	AAA	AAG	CAA	CTG	TGG	CCA	ATC	TCT	ATC	TTT	ATT	GCA	GCA	459	
Ile	Gln	Lys	Lys	Glu	Leu	Trp	Gly	Ile	Cys	Ile	Phe	Ile	Ala	Ala			
		95				100				105							
GTT	GAC	CTA	CAT	GAG	ATC	TCG	TTC	ACT	TTT	ACT	GAG	CTA	CAG	AAA	AAC	507	
Val	Asp	Leu	Asp	Glu	Met	Ser	Phe	Thr	Thr	Phe	Thr	Glu	Leu	Gln	Lys	Asn	
		110				115				120							
ATA	GAA	ATC	AGT	GTC	CAT	AAA	TTC	TTT	AAC	TTA	CTA	AAA	GAA	ATT	CAT	555	
Ile	Glu	Ile	Ser	Val	His	Lys	Phe	Phe	Asn	Leu	Leu	Lys	Glu	Ile	Asp		
		125				130				135							
ACC	ACT	ACC	AAA	CTT	CAT	AAT	GCT	ATC	TCA	AGA	CTG	TTC	AAG	AAC	TAT	603	
Thr	Ser	Thr	Lys	Val	Asp	Asn	Ala	Met	Ser	Arg	Leu	Leu	Lys	Lys	Tyr		
		140				145				150				155			
GAT	CTA	TTG	TTT	GCA	CTC	TTC	AGC	AAA	TTG	CAA	AGG	ACA	TGT	CAA	CTT	651	
Asp	Val	Leu	Phe	Ala	Leu	Phe	Ser	Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu		
		160				165				170							

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ATA TAT TTG ACA CAA CCC ACC ACT TCG ATA TCT ACT GAA ATA AAT TCT	699		
Ile Tyr Leu Thr Cln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser			
175	180	185	
GCA TTG GTG CTA AAA CTT TCT TCG ATC ACA TTT TTA TTA GCT AAA CGG	747		
Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly			
190	195	200	
GAA CTA TTA CAA ATC GAA GAT CAT CTC GTC ATT TCA TTT CAG TTA ATC	795		
Glu Val Leu Cln Met Glu Asp Asp Leu Val Ile Ser Phe Cln Leu Met			
205	210	215	
CTA TCT CTC CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATC TTG CTC	843		
Leu Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu			
220	225	230	235
AAA GAA CCA TAT AAA ACA GCT CTT ATA CCC ATT AAT GCT TCA CCT CGA	891		
Lys Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg			
240	245	250	
ACA CCC ACC CGA CGT CAG AAC ACC AGT GCA CGG ATA GCA AAA CAA CTA	939		
Thr Pro Arg Arg Gly Cln Asn Arg Ser Ala Arg Ile Ala Lys Cln Leu			
255	260	265	
GAA AAT GAT ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA GAT CAA TCT	987		
Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys			
270	275	280	
AAT ATA GAT GAC CTC AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT	1035		
Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe			
285	290	295	
ATG AAT TCT CTT CGA CTT GTC ACA TCT AAT GCA CTT CCA GAG GTT GAA	1083		
Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu			
300	305	310	315
AAT CTT TCT AAA CGA TAC GAA CAA ATT TAT CTT AAA AAT AAA GAT CTA	1131		
Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu			
320	325	330	
GAT GCA AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT	1179		
Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Cln Thr Asp Ser			
335	340	345	
ATA GAC AGT TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT	1227		
Ile Asp Ser Phe Glu Thr Cln Arg Thr Pro Arg Lys Ser Asn Leu Asp			
350	355	360	
GAA GAG GTG AAT CTA ATT CCT CCA CAC ACT CCA CTT AGG ACT GTT ATC	1275		
Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met			
365	370	375	

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AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA ACT CAT CAA	1323
Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln	
380	385
390	395
CCT TCA GAA AAT CTC ATT TCC TAT TTT AAC AAC TGC ACA GTC AAT CCA	1371
Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro	
400	405
410	
AAA CAA ACT ATA CTC AAA AGA CTG AAG GAT ATA CGA TAC ATC TTT AAA	1419
Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys	
415	420
425	
GAG AAA TTT CCT AAA CCT GTG GGA CAG CCT TGT GTC GAA ATT CGA TCA	1467
Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser	
430	435
440	
CAG CGA TAC AAA CTT CGA GTT CGC TTG TAT TAC CGA GTC ATC GAA TCC	1515
Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser	
445	450
455	
ATG CTT AAA TCA GAA GAA CGA TTA TCC ATT CAA AAT TTT ACC AAA	1563
Met Leu Lys Ser Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys	
460	465
470	475
CTT CTC AAT GAC AAC ATT TTT CAT ATG TCT TTA TTG CGG TGC CCT CTT	1611
Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu	
480	485
490	
GAG CTT CTA ATC GCC ACA TAT ACC AGA AGT ACA TCT CAG AAT CTT GAT	1659
Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp	
495	500
505	
TCT CGA ACA CAT TTG TCT TTC CGA TGG ATT CTC AAT GTC CTT AAT TTA	1707
Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu	
510	515
520	
AAA CCC TTT CAT TTT TAC AAA CTG ATC GAA ACT TTT ATC AAA CCA GAA	1755
Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu	
525	530
535	
GCC AAC TTG ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT	1803
Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His	
540	545
550	555
CGA ATC ATG CAA TCC CTT CGA TGG CTC TCA GAT TCA CCT TTA TTT GAT	1851
Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp	
560	565
570	
CTT ATT AAA CAA TCA AAG GAC CGA GAA CGA ACT GAT GAC CTT GAA	1899
Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu	
575	580
585	

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TCT GCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT CCA GCA 1947
 Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala
 590 595 600

GAT ATC TAT CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT 1995
 Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr
 605 610 615

ACG CCT GTA AAT TCT ACT GCA AAT CCA CAG ACA CAA CCA ACC TCA CCC 2043
 Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala
 620 625 630 635

TTC CAG ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTC TTT TAT 2091
 Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr
 640 645 650

AAA AAA CTG TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA 2139
 Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu
 655 660 665

CGC CTT CTG TCT GAG CAC CCA GAA TTA CAA CAT ATC ATC TGG ACC CTT 2187
 Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu
 670 675 680

TTC CAG CAC ACC CTC CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT 2235
 Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His
 685 690 695

TTC CAC CAA ATT ATG ATG TGT TCC ATG TAT CGC ATA TGC AAA GTG AAG 2283
 Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys
 700 705 710 715

AAT ATA GAC CTT AAA TTC AAA ATC ATT GTA ACA GCA TAG AAG GAT CTT 2331
 Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu
 720 725 730

CCT CAT GCT GTT GAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG 2379
 Pro His Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu
 735 740 745

GAG TAT GAT TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG ACA 2427
 Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg
 750 755 760

CTG AAA ACA AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTC 2475
 Leu Lys Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu
 765 770 775

TCA CCA ATA CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA 2523
 Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser
 780 785 790 795

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PATENT

CCC TTA CGG ATT CCT CGA CGG AAC ATC TAT ATT TCA CCC CTG AAG ACT 2571
 Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser
 800 805 810

CCA TAT AAA ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA 2619
 Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro
 815 820 825

AGA TCA AGA ATC TTA GCA ATT CCT GAA TCA TTC CGG ACT TCT GAC 2667
 Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu
 830 835 840

AAG TTC CAC AAA ATA AAT CAG ATG GTC TGT AAC AGC GAC CGT GTG CTC 2715
 Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu
 845 850 855

AAA AGA AGT CCT GAA CGA AGC AAC CCT CCT AAA CCA CTC AAA AAA CTA 2763
 Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu
 860 865 870 875

CCC TTT CAT ATT GAA CGA TCA CAT GAA CCA CAT GGA ACT AAA CAT CTC 2811
 Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu
 880 885 890 890

CGA CGA GAG TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT 2859
 Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr
 895 900 905

CGA ACA CGA ATC CAA AAC CAG AAA ATG AAT CAT ACC ATC GAT ACC TCA 2907
 Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser
 910 915 920

AAC AAC GAA GAC AAA TCAGGATCTC AGGACCTTGG TCGACACTGT GTACACCTCT 2962
 Asn Lys Glu Glu Lys
 925

GGATTCAATTG TCTCTCACAG ATGTGACTGT AT 2994
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Please insert the accompanying paper copy of the Sequence Listing, page numbers 1 to 10, at the end of the application.